Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:09:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525128.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10525128 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525128.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:09:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	559,602
Mapped reads	500,471 / 89.43%
Unmapped reads	59,131 / 10.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,616 / 2.43%
Read min/max/mean length	30 / 101 / 101.89
Duplicated reads (estimated)	9,962 / 1.78%
Duplication rate	1.21%
Clipped reads	513,017 / 91.68%

2.2. ACGT Content

Number/percentage of A's	9,938,966 / 26.06%
Number/percentage of C's	7,693,610 / 20.17%
Number/percentage of T's	11,888,132 / 31.17%
Number/percentage of G's	8,622,856 / 22.61%
Number/percentage of N's	1,501 / 0%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0123

Standard Deviation	0.1613

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

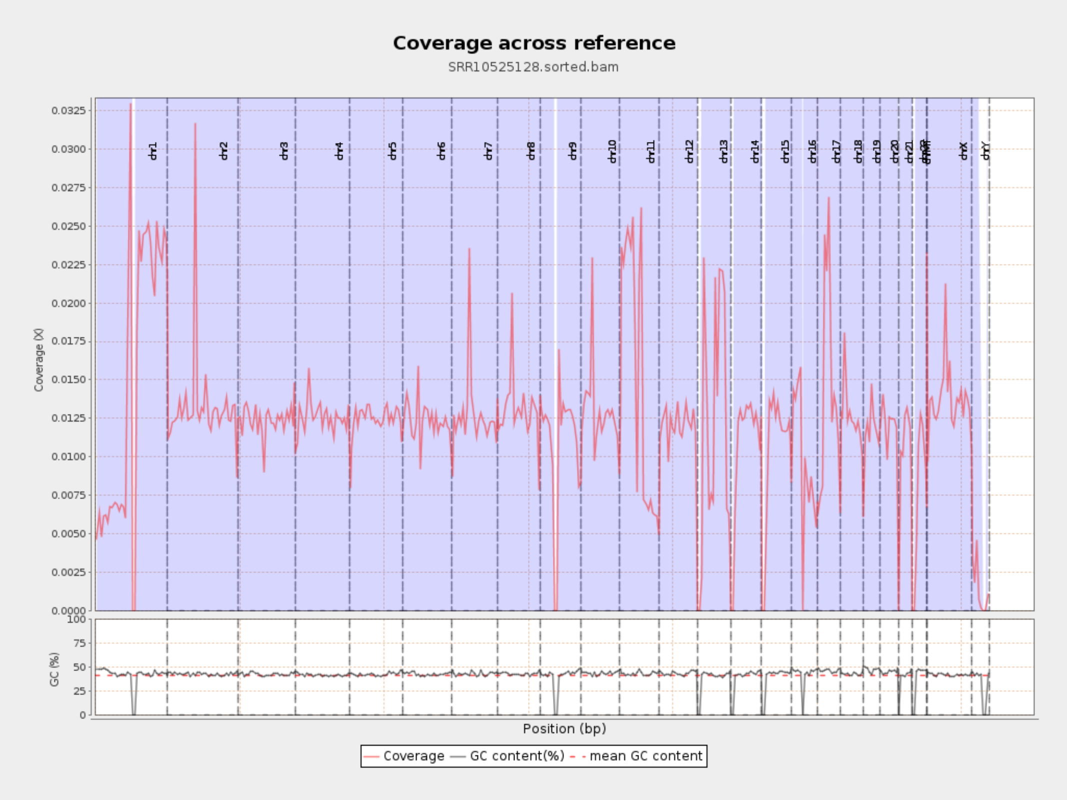
General error rate	0.79%
Mismatches	293,554
Insertions	3,678
Mapped reads with at least one insertion	0.73%
Deletions	8,827
Mapped reads with at least one deletion	1.74%
Homopolymer indels	43.4%

2.6. Chromosome stats

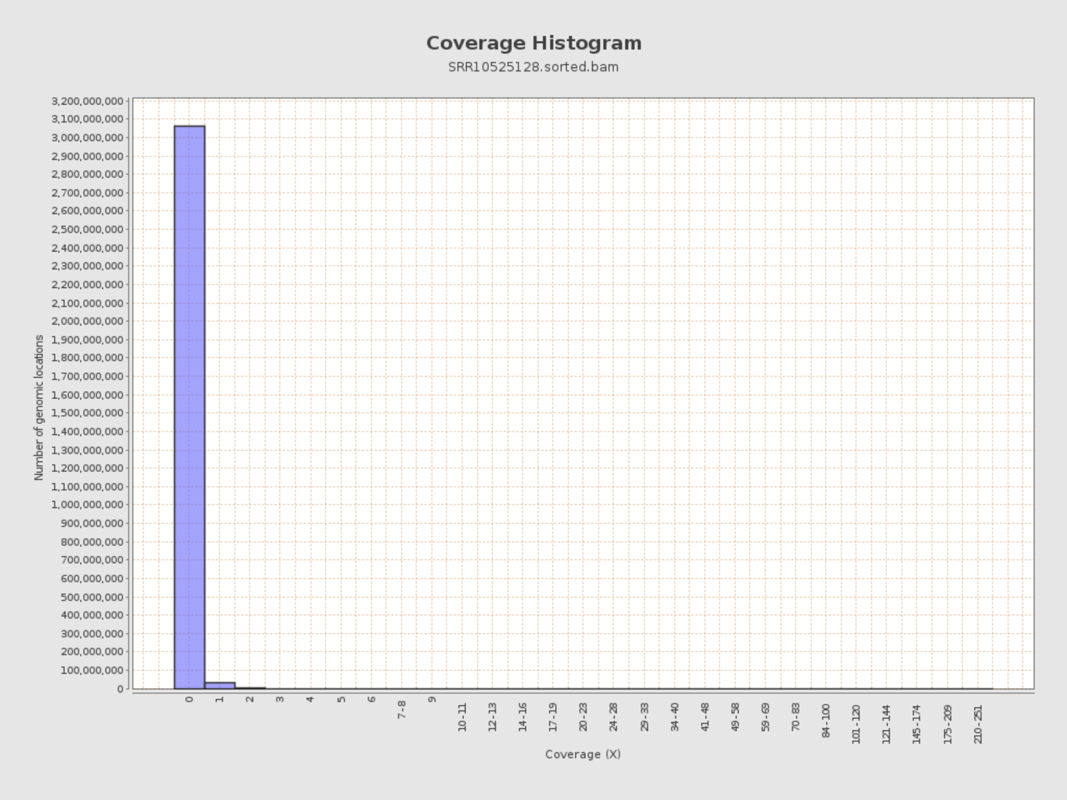
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3632546	0.0146	0.2508
chr2	243199373	3241446	0.0133	0.2173
chr3	198022430	2445106	0.0123	0.1154
chr4	191154276	2404187	0.0126	0.1186
chr5	180915260	2270395	0.0125	0.1167
chr6	171115067	2107457	0.0123	0.1242
chr7	159138663	2027107	0.0127	0.2113

chr8	146364022	1913529	0.0131	0.1934
chr9	141213431	1549424	0.011	0.1523
chr10	135534747	1761980	0.013	0.1609
chr11	135006516	2086292	0.0155	0.179
chr12	133851895	1612146	0.012	0.1142
chr13	115169878	1353488	0.0118	0.1122
chr14	107349540	1127138	0.0105	0.1117
chr15	102531392	1056192	0.0103	0.1047
chr16	90354753	860008	0.0095	0.107
chr17	81195210	1154881	0.0142	0.1346
chr18	78077248	990963	0.0127	0.2247
chr19	59128983	696539	0.0118	0.1891
chr20	63025520	754776	0.012	0.1145
chr21	48129895	494271	0.0103	0.1107
chr22	51304566	392417	0.0076	0.0905
chrMT	16571	386	0.0233	0.1508
chrX	155270560	2145500	0.0138	0.1414
chrY	59373566	82079	0.0014	0.0454

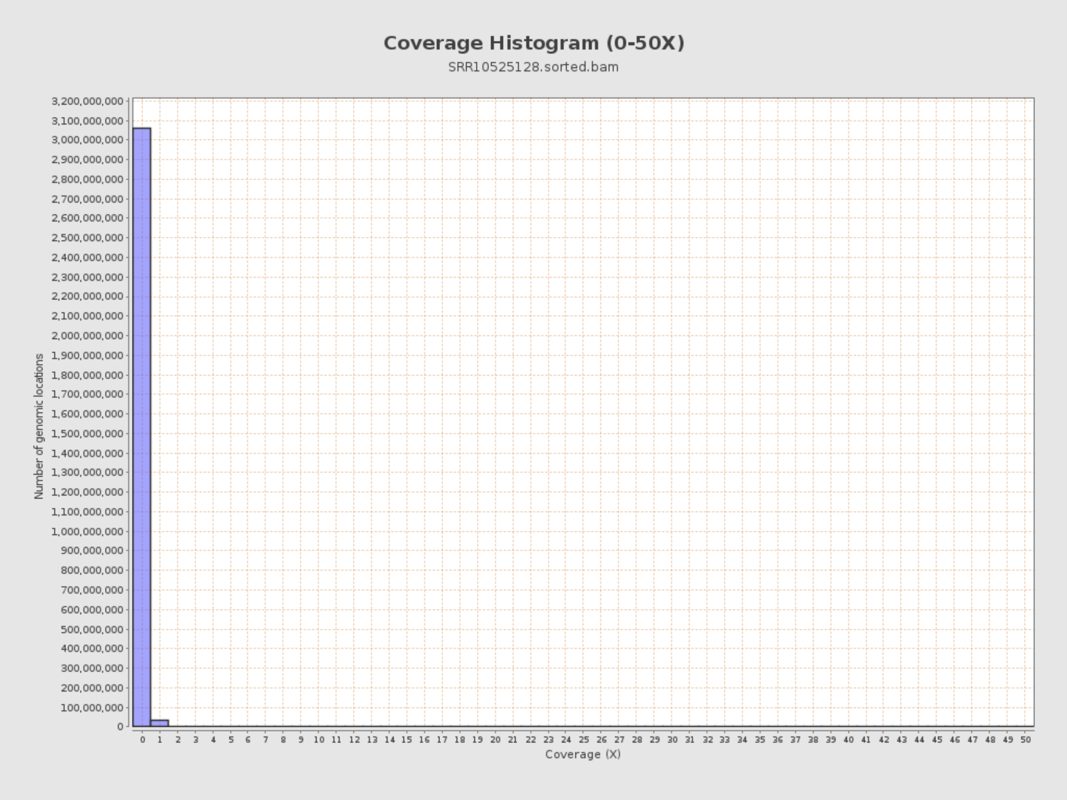
3. Results : Coverage across reference



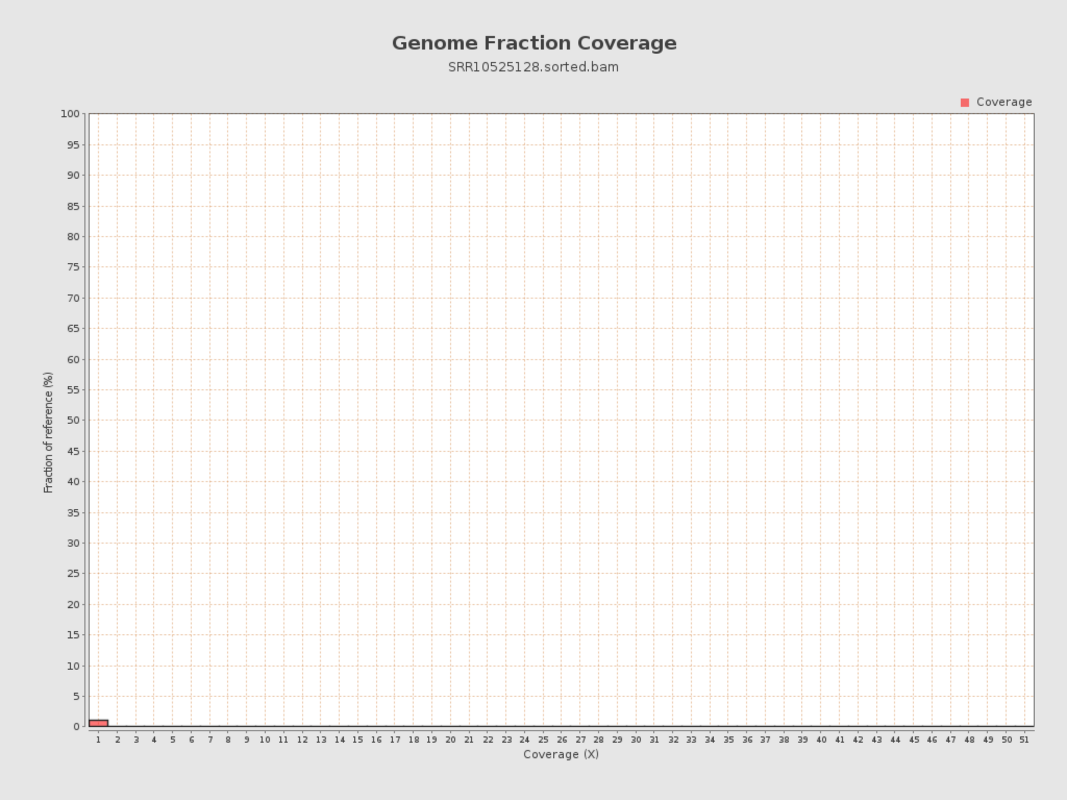
4. Results : Coverage Histogram



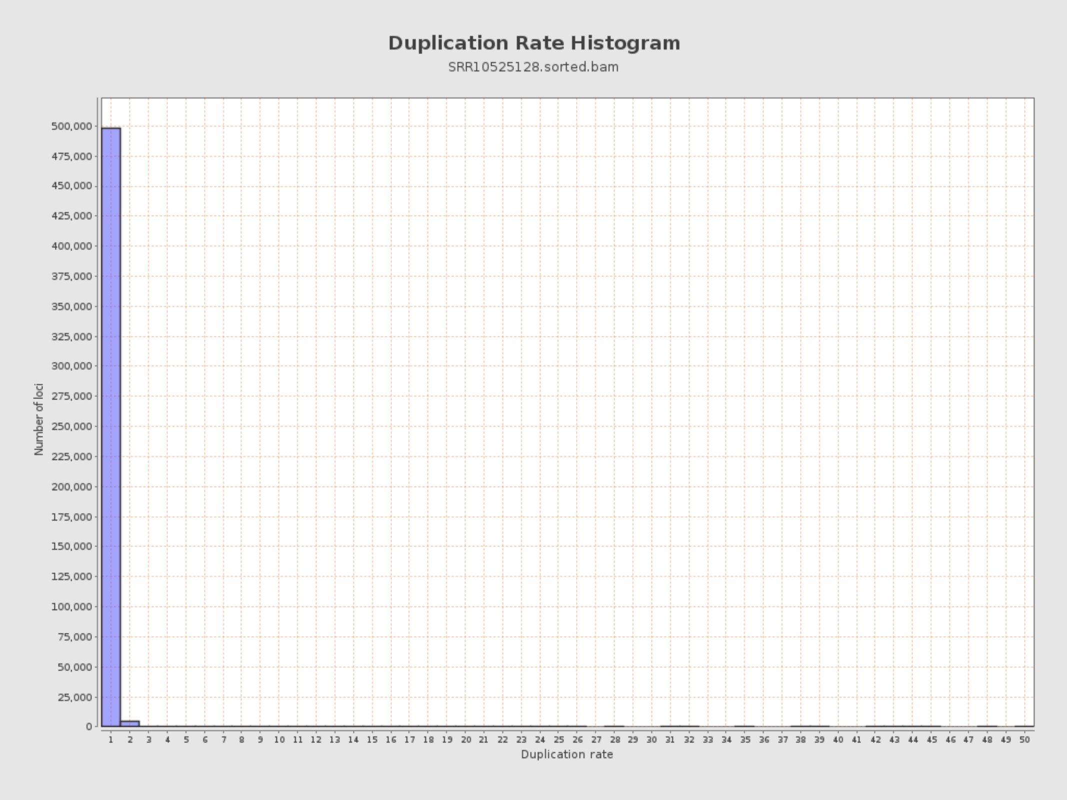
5. Results : Coverage Histogram (0-50X)



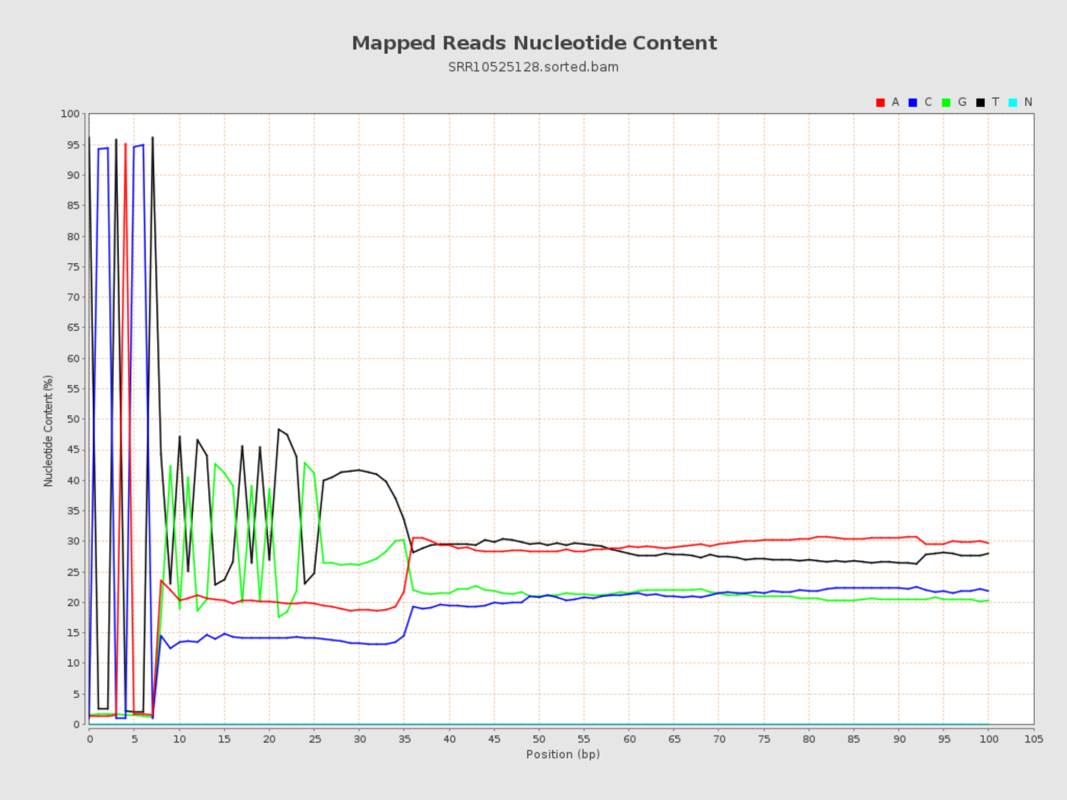
6. Results : Genome Fraction Coverage



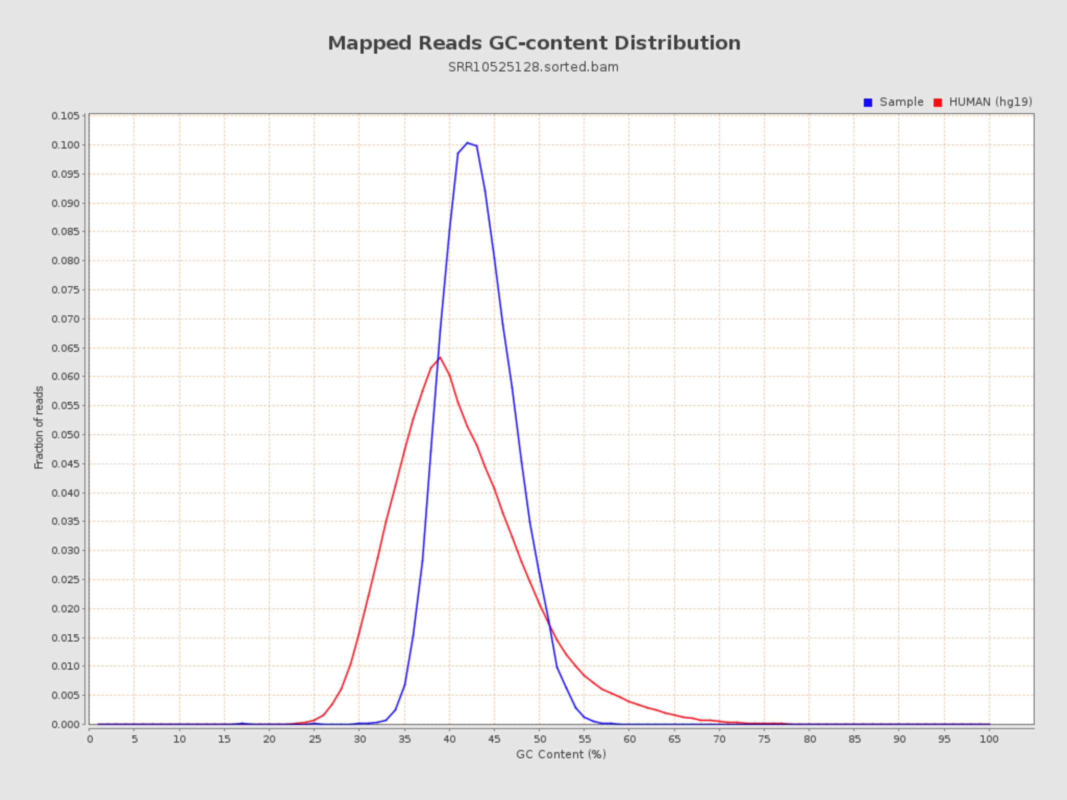
7. Results : Duplication Rate Histogram



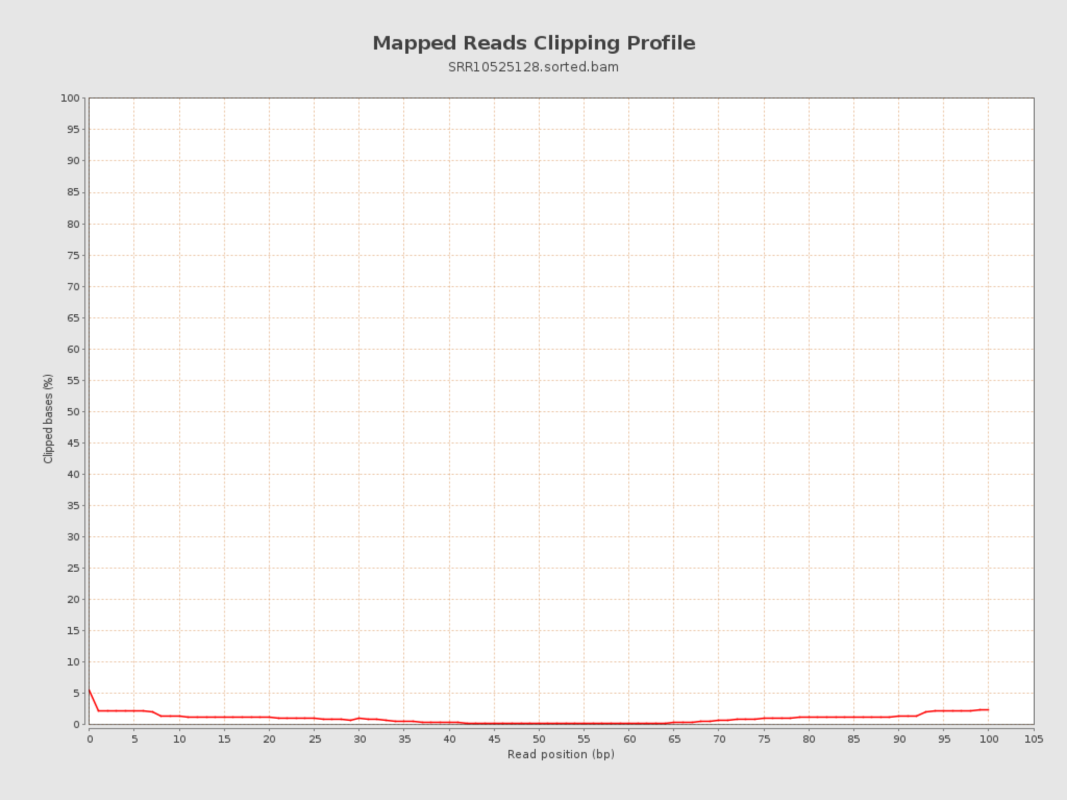
8. Results : Mapped Reads Nucleotide Content



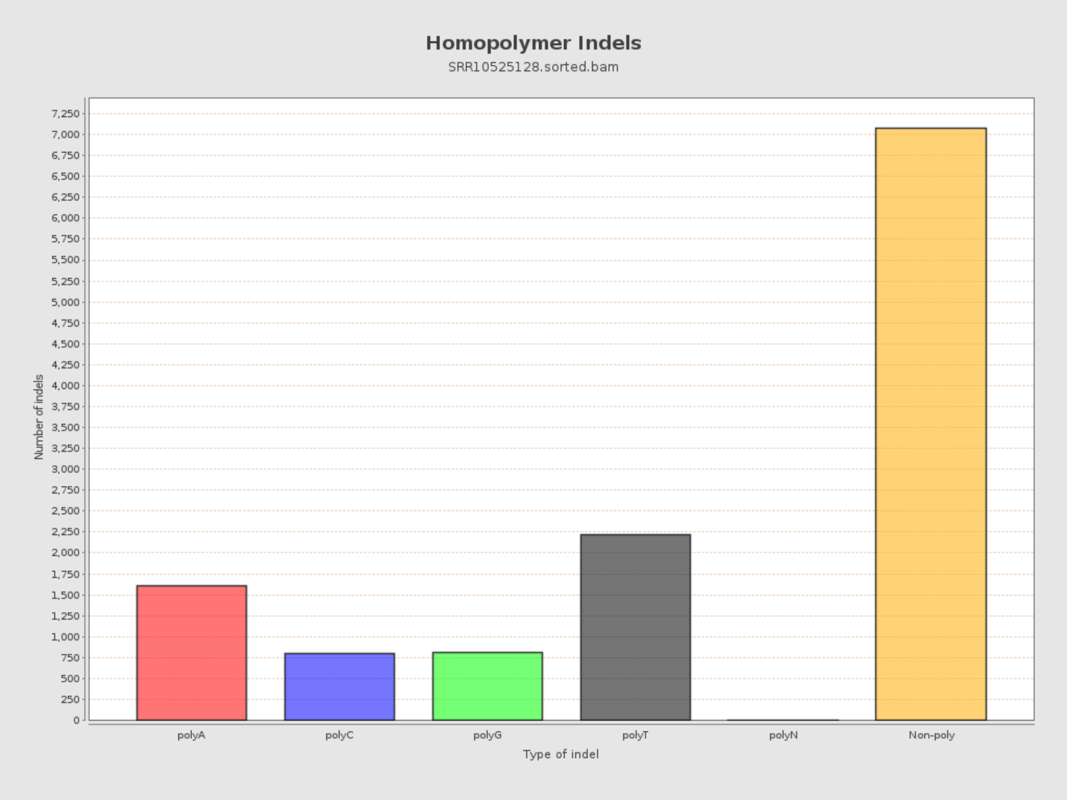
9. Results : Mapped Reads GC-content Distribution



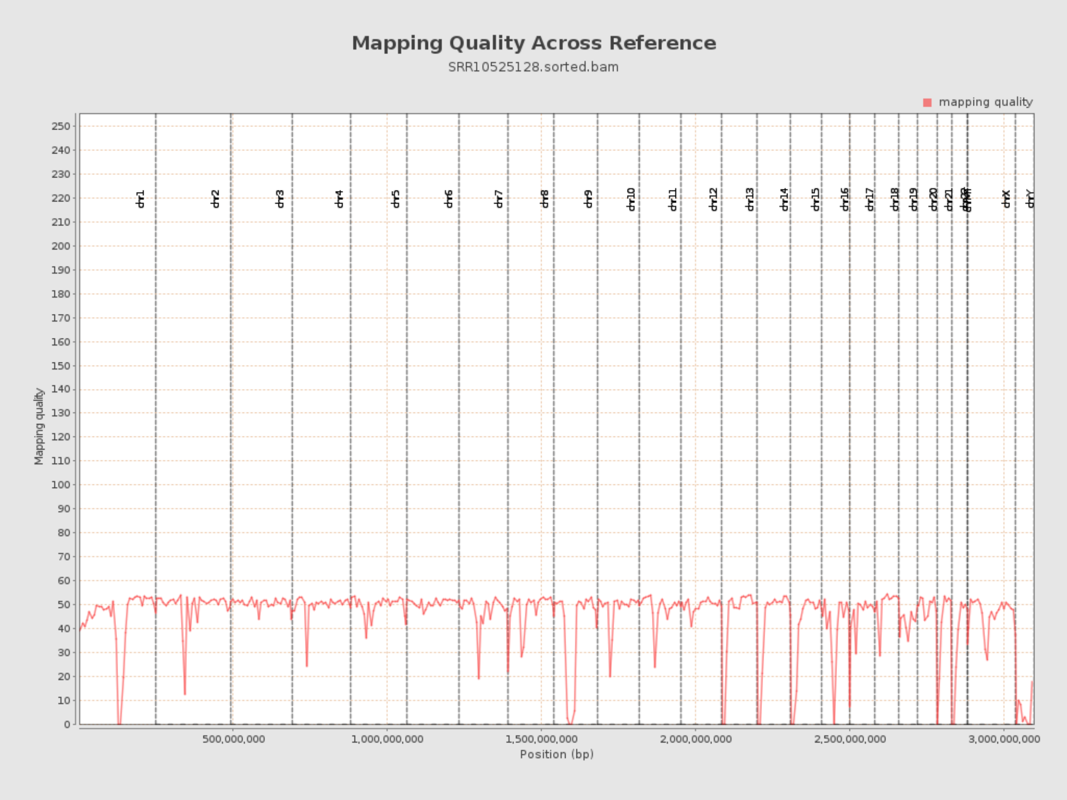
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram